IN THE SPECIFICATION

Please replace the paragraph beginning on page 27, line 7 with the following amended paragraph:

Figures 105A-105C depicts an alignment of Env polypeptides from various HIV isolates (SEQ ID NOS:143-147). The regions between the arrows indicate regions (of TV1 and TV2 clones) in the beta and/or bridging sheet region(s) that can be deleted and/or truncated. The "*" denotes N-linked glycosylation sites (of TV1 and TV2 clones), one or more of which can be modified (*e.g.*, deleted and/or mutated).

Please replace the paragraph beginning on page 36, line 6 with the following amended paragraph:

For example, percent identity of a particular nucleotide sequence to a reference sequence can be determined using the homology algorithm of Smith and Waterman with a default scoring table and a gap penalty of six nucleotide positions. Another method of establishing percent identity in the context of the present invention is to use the MPSRCH package of programs copyrighted by the University of Edinburgh, developed by John F. Collins and Shane S. Sturrok, and distributed by IntelliGenetics, Inc. (Mountain View, CA). From this suite of packages, the Smith-Waterman algorithm can be employed where default parameters are used for the scoring table (for example, gap open penalty of 12, gap extension penalty of one, and a gap of six). From the data generated, the "Match" value reflects "sequence identity." Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, such as the alignment program BLAST, which can also be used with default parameters. For example, BLASTN and BLASTP can be used with the following default parameters: genetic code = standard; filter = none; strand = both; cutoff = 60; expect = 10; Matrix = BLOSUM62; Descriptions = 50 sequences; sort by = HIGH SCORE; Databases = non-redundant, GenBank + EMBL + DDBJ + PDB + GenBank CDS translations + Swiss

protein + Spupdate + PIR. Details of these programs can be found at the following internet address: ~~http://www.~~ncbi.nlm.gov/cgi-bin/BLAST.

Please replace the paragraph beginning on page 50, line 6 with the following amended paragraph:

Gag sequence obtained from other Type C HIV-1 variants may be manipulated in similar fashion following the teachings of the present specification. Such other variants include, but are not limited to, Gag protein encoding sequences obtained from the isolates of HIV-1 Type C, for example as described in Novitsky et al., (1999), *supra*; Myers et al., *infra;* Virology, 3rd Edition (W.K. Joklik ed. 1988); *Fundamental Virology*, 2nd Edition (B.N. Fields and D.M. Knipe, eds. 1991); *Virology*, 3rd Edition (Fields, BN, DM Knipe, PM Howley, Editors, 1996, Lippincott-Raven, Philadelphia, PA and on the World Wide Web (Internet), for example at ~~http://~~hiv-web.lanl.gov/cgi-bin/hivDB3/public/wdb/ssampublic and ~~http://~~hiv-web.lanl.gov.

Please replace the paragraph beginning on page 95, line 15 with the following amended paragraph:

Furthermore selected B- and/or T-cell epitopes can be added to the Pol constructs (*e.g.*, 3' of the truncated INT or within the deletions of the RT- and INT-coding sequence) to replace and augment any epitopes deleted by the functional modifications of RT and INT. Alternately, selected B- and T-cell epitopes (including CTL epitopes) from RT and INT can be included in a minimal VLP formed by expression of the synthetic Gag or synthetic Pol cassette, described above. (For descriptions of known HIV B- and T-cell epitopes see, HIV Molecular Immunology Database CTL Search Interface; Los Alamos Sequence Compendia, 1987-1997;Internet address: ~~http://~~hiv-web.lanl.gov/immunology/index.html.)

Please replace Table 4 on page 107 with the following amended Table 4:

Table 4

Leader	Amino acid sequence	DNA sequence
WTnative (8_2_TV1_C.ZA)	MRVMGTQKNCQQWWIWGIL GFWMLMIC (SEQ ID NO:136)	ATGAGAGTGATGGGGACACAGAA GAATTGTCAACAATGGTGGATAT GGGGCATCTTAGGCTTCTGGATG CTAATGATTTGT (SEQ ID NO:137)
WTmod (8_2_TV1_C.ZA)	MRVMGTQKNCQQWWIWGIL GFWMLMIC (SEQ ID NO:1368)	ATGCGCGTGATGGGCACCCAGAA GAACTGCCAGCAGTGGTGGATCT GGGGCATCCTGGGCTTCTGGATG CTGATGATCTGC (SEQ ID NO:1389)
Tpa1	MDAMKRGLCCVLLLCGAVFV SPSAS (SEQ ID NO:139~~140~~)	ATGGATGCAATGAAGAGAGGGCT CTGCTGTGTGCTGCTGCTGTGTGG AGCAGTCTTCGTTTCGCCCAGCGC CAGC (SEQ ID NO:140~~1~~)
Tpa2	MDAMKRGLCCVLLLCGAVFVSPS (SEQ ID NO:141~~2~~)	ATGGATGCAATGAAGAGAGGGCT CTGCTGTGTGCTGCTGCTGTGTGG AGCAGTCTTCGTTTCGCCCAGC (SEQ ID NO:142~~3~~)